

=> d hist

(FILE 'HOME' ENTERED AT 12:51:04 ON 03 SEP 2004)

FILE 'MEDLINE, EMBASE, BIOSIS, CAPLUS' ENTERED AT 12:51:24 ON 03 SEP 2004

L1 1257 S CDC25A  
L2 62 S L1 (S) MAMMAL?  
L3 101205 S ANTISENSE OR ANTIGENE  
L4 1 S L2 (S) L3  
L5 4 S L2 (P) L3  
L6 2 S L2 (S) (TYROSINE PHOSPHATASE)  
L7 4 S L2 AND L3  
L8 1 DUP REM L7 (3 DUPLICATES REMOVED)  
L9 2 DUP REM L6 (0 DUPLICATES REMOVED)  
L10 1 S L4 NOT L8  
L11 3869 S CDC25  
L12 320 S L11(2A)YEAST  
L13 0 S L12(2A)DEFICIENT  
L14 4 S L11 (2A) DEFICIENT  
L15 4 S L14(S)YEAST  
L16 1 DUP REM L15 (3 DUPLICATES REMOVED)  
L17 17 S L1 (S) L3  
L18 8 DUP REM L17 (9 DUPLICATES REMOVED)  
L19 0 S L15 AND ANTISENSE  
L20 9 S L11 (S) L3  
L21 6 DUP REM L20 (3 DUPLICATES REMOVED)

=> logoff hold

## SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 75.70

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.